Genetic diversity of[i] Rhizoctonia solani[/i] associated with potato tubers in France

Marie Fiers, Veronique Edel-Hermann, Cécile Héraud, Nadine Gautheron, Catherine Chatot, Yves Le Hingrat, Karima Bouchek-Mechiche, Christian Steinberg

Genetic diversity of *Rhizoctonia solani* associated with potato tubers in France

Marie FIERS[1], Véronique EDEL-HERMANN[1], **Cécile HERAUD**[1], Nadine GAUTHERON[1], Catherine CHATOT[2], Yves LE HINGRAT[3], Karima BOUCHEK-MECHICHE[1], Christian STEINBERG*[1]

[1]INRA-National Institute of Agronomical Research/University of Burgundy
UMR 1229 MSE Microbiology of Soil and Environment
17 rue Sully, F-21000 Dijon, Dijon, France.
[2] Germicopa R&D, Kerguivarch, 29520 Châteauneuf du Faou, France
[3] FNPPPT, Roudouhir, 29460 Hanvec, France

*E-mail : christian.steinberg@dijon.inra.fr

The **hidden polymorphism** of a fungal group can be revealed thanks to the use of different molecular approaches. In the case of *Rhizoctonia solani* (teleomoph *Thanatephorus cucumeris*, Kühn, 1858), the diversity of 73 French strains isolated from potato tubers grown in the mains potato seed production areas in France and 31 strains isolated in 9 other countries was assessed. **Three molecular tools** are proposed to investigate different levels of diversity within this **fungal collection:** sequencing of the ITS region, sequencing of a part of the gene *tef-1α*, and AFLP analysis of the total DNA.

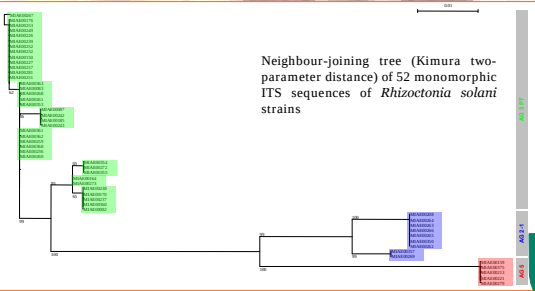
The isolates are stored in the collection "Microorganisms of Interest for Agriculture and Environment" (MIAE, INRA Dijon, France, see Heraud *et al.*, Poster 24 Area 4 for more details).

A sclerotia (black scurf)
B skinning
C enlarged lenticels

Alterations where *R. solani* was isolated

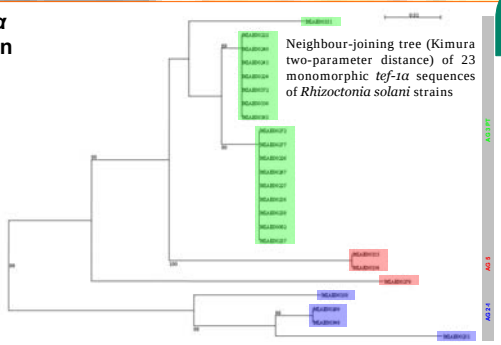
DNA SEQUENCE ANALYSIS

Internal Transcribed Spacer sequences (ITS1 and ITS2) of ribosomal DNA (rDNA)



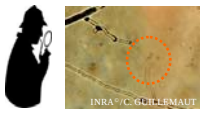
Neighbour-joining tree (Kimura two-parameter distance) of 52 monomorphic ITS sequences of *Rhizoctonia solani* strains

Part of the gene *tef-1α* coding for an Elongation Factor (EF)



Neighbour-joining tree (Kimura two-parameter distance) of 23 monomorphic *tef-1α* sequences of *Rhizoctonia solani* strains

Classical (= microscopic) method used to determine AG is laborious, time-consuming and requires technical training.



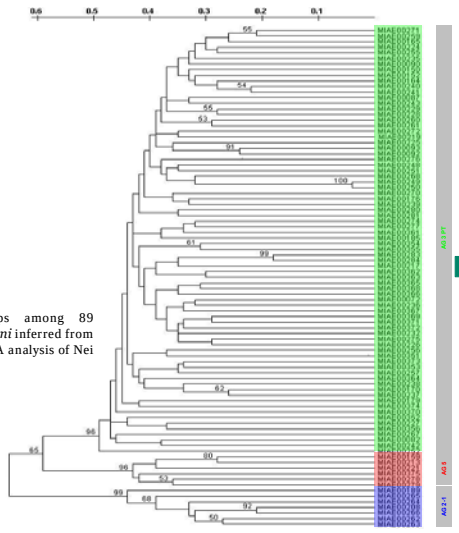
C2 type (= killing reaction) anastomosis based on the fusion the hyphal tips of two compatible individuals belonging to the same AG (McNish *et al.*, 1993)

	AG[1] diversity		Number of types	
	inter-	intra-	monomorphic	polymorphic
ITS	+	+-	10	29
EF	+	+	7	30

[1] Anastomosis Group

TOTAL DNA ANALYSIS

Amplified Fragment Length Polymorphism (AFLP) analysis: total DNA fingerprints



Phylogenetic relationships among 89 strains of *Rhizoctonia solani* inferred from AFLP data using a UPGMA analysis of Nei – Li distances

- ► **Significant diversity**
- ► **No particular structure of the studied populations**
- ► **No relation between the genetic profiles of the strains and their geographical origin**

Level of polymorphism

METHODOLOGICAL CONCLUSIONS

✓ **Validation of the molecular method** to determine AG.

✓ Target sequences DNA vs. Total DNA analysis highlight **different but complementary** informations:

☞ sequencing: rapid access to AG (sub-)group

☞ AFLP: high discrimination between strains.

SCIENTIFIC CONCLUSIONS

✓ **High intra-species and intra-AG diversity** of the French strains of *R. solani*.

✓ **Constant evolution of the genomes** according to the genetic events in the environment.

✓ **Polymorphic sites** within strains probably due to several copies of ITS and gene *tef-1α* within the same nucleus or between different nuclei of *R. solani* strains.

Keywords : amplified fragment length polymorphism, anastomosis group, elongation factor, internal transcribed spacer, polymorphic group